

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10 507,343
Source: PCT
Date Processed by STIC: 4-28-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/28/2005

PATENT APPLICATION: US/10/507,343

TIME: 16:23:13

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Output Set: N:\CRF4\04272005\J507343.raw

3 <110> APPLICANT: Ema, Hideo
 4 Nakauchi, Hiromitsu
 5 Osawa, Mitsujiro
 7 <120> TITLE OF INVENTION: PROTEIN SUSTAINING UNDIFFERENTIATED STEM CELLS
 9 <130> FILE REFERENCE: 790086.405USPC
 11 <140> CURRENT APPLICATION NUMBER: US 10/507,343
 C--> 12 <141> CURRENT FILING DATE: 2004-09-10
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP02/02265
 15 <151> PRIOR FILING DATE: 2002-03-11
 17 <160> NUMBER OF SEQ ID NOS: 27
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1140
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Mus musculus
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 28 ctgctcctgc tgcgagcggga tgcagggcag ccacctgagg agagcttgta cctgtggatc 120
 29 gacgcccatac aggctagagt gctcatagga tttgaagaag acattctgat tgtctcggag 180
 30 gggaaaatgg ccccttttac acatgatttc aggaaagccc aacaaagaat gccagccatt 240
 31 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggc agaatacttc 300
 32 tacgagttcc tgtctctgcg ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
 33 gtccctttgc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg ttcccgtgt 420
 34 ctcggaacac aagacggggt agcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
 35 ggcaaacacca tccttaggac ccctcagaat gccatcttct ttaaaacatg tcaacaagct 540
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 37 ccggatgggt tctacgggcc tactgtgag aaagccctgt gcataccccg atgtatgaac 660
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 40 aaatgtattt gccctcctgg actcgaggga gagcagtggt aactcagcaa atgccccaa 840
 41 ccctgccgaa atggaggtaa atgcattggt aaaagcaagt gtaagtgcc gaaaggttac 900
 42 caaggagacc tgtgtcttaa gcccgctgc gagcctggct gtggtgcccc cggaacctgc 960
 43 cacgaaccca acaagtgcc gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
 44 tatggagcca gcctcatgca tgccccgagg ccagcaggcg ccgggctgga gcgacacacg 1080
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 49 <211> LENGTH: 379
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Mus musculus
 53 <400> SEQUENCE: 2
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 55 1 5 10 15
 57 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro

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60 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
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63 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
64          50          55          60
66 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
67 65          70          75          80
69 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
70          85          90          95
72 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
73          100          105          110
75 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
76          115          120          125
78 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
79          130          135          140
81 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
82 145          150          155          160
84 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
85          165          170          175
87 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
88          180          185          190
90 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
91          195          200          205
93 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
94          210          215          220
96 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
97 225          230          235          240
99 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
100          245          250          255
102 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
103          260          265          270
105 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
106          275          280          285
108 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
109          290          295          300
111 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
112 305          310          315          320
114 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
115          325          330          335
117 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
118          340          345          350
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124          370          375
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 1140
129 <212> TYPE: DNA
130 <213> ORGANISM: Homo sapiens

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132 <400> SEQUENCE: 3

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135 gatgtccacc aggcaagagt actcatagga tttgaagaag atatcctgat tgtttcagag 180
136 gggaaaatgg caccttttac acatgatttc agaaaagcgc aacagagaat gccagctatt 240
137 cctgtcaata tccattccat gaattttacc tggcaagctg cagggcaggc agaatacttc 300
138 tatgaattcc tgtccttgcg ctccctggat aaaggcatca tggcagatcc aaccgtcaat 360
139 gtccctctgc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg tttcccatgt 420
140 cttggaaaac aggatggggt ggcagcattt gaagtggatg tgattgttat gaattctgaa 480
141 ggcaacacca ttctccaaac acctcaaaat gctatcttct ttaaaacatg tctacaagct 540
142 gagtgcccg gcgggtgccg aaatggaggc ttttgtaatg aaagacgcat ctgcgagtgt 600
143 cctgatgggt tccacggacc tcaactgtgag aaagcccttt gtacccacg atgtatgaat 660
144 ggtggacttt gtgtgactcc tggtttctgc atctgccac ctggattcta tggagtgaac 720
145 tgtgacaaag caaactgctc aaccacctgc tttaatggag ggacctgttt ctacctgga 780
146 aaatgtattt gccctccagg actagaggga gagcagtggt aaatcagcaa atgccacaa 840
147 ccctgtcgaa atggaggtaa atgcattggt aaaagcaaat gtaagtgttc caaaggttac 900
148 caggagagacc tctgttcaaa gcctgtctgc gagcctggct gtggtgcaca tggaaacctgc 960
149 catgaacca acaaatgcca atgtcaagaa ggttggcatg gaagacactg caataaaagg 1020
150 tacgaagcca gcctcatata tgccctgagg ccagcaggcg cccagctcag gcagcacacg 1080
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154 <210> SEQ ID NO: 4

155 <211> LENGTH: 379

156 <212> TYPE: PRT

157 <213> ORGANISM: Homo sapiens

159 <400> SEQUENCE: 4

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164 20 25 30
166 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
167 35 40 45
169 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
170 50 55 60
172 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
173 65 70 75 80
175 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
176 85 90 95
178 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
179 100 105 110
181 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
182 115 120 125
184 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
185 130 135 140
187 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
188 145 150 155 160
190 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
191 165 170 175
193 Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
194 180 185 190

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196 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
197      195      200      205
199 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
200      210      215      220
202 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
203 225      230      235      240
205 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
206      245      250      255
208 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
209      260      265      270
211 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
212      275      280      285
214 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
215      290      295      300
217 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
218 305      310      315      320
220 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
221      325      330      335
223 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
224      340      345      350
226 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
227      355      360      365
229 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
230      370      375

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233 <210> SEQ ID NO: 5

234 <211> LENGTH: 1098

235 <212> TYPE: DNA

236 <213> ORGANISM: Rattus norvegicus

238 <400> SEQUENCE: 5

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241 gacgcccatac aggccagagt actcatagga tttgaagaag atattctgat tgtctcggag 180
242 gggaaaatgg ccccttttac acatgatttc aggaaagccc aacaaagaat gccagccatt 240
243 cccgtcaata tccactccat gaattttacc tggcaagctt cagggcaggc agagtacttc 300
244 tatgagttcc tgtcgtgctg ctcgctggat aaaggcatca tggcagaccc aactgtcaat 360
245 gtccctcggc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg tttcccggtg 420
246 ctcggaacaac aggatggggt ggcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
247 ggcaacccca tccttcggac ccctcaaaat gctatcttct ttaaaacatg tcaacaagct 540
248 gagtgcccag gaggggtgtcg aaatggaggc ttttgtaacg aaaggcgggt ctgcgagtgt 600
249 cccgatgggt tctatggacc tctactgtgag aaagccctct gcatacctcg atgtatgaac 660
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251 tgtgacaaaag caaactgctc ggccacctgc tttaatggag ggacctgttt ttaccaggga 780
252 aaatgtatatt gccctccagg acttgaggga gagcagtgtg aactcagcaa gtgcccccaa 840
253 ccctgccgaa acggaggtaa atgcattggt aaaagcaagt ctgtctgcga gcctggctgc 900
254 ggtgcccata gaacctgcca cgaacccaac aaatgccagt gtcgagaggg ctggcatggg 960
255 agacactgca ataaaaggta cggagccagc ctcatgcatg ccccgaggcc agcaggcgcc 1020
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260 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING

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Input Set : E:\405uspc.app.txt

Output Set: N:\CRF4\04272005\J507343.raw

261 <211> LENGTH: 365

262 <212> TYPE: PRT

263 <213> ORGANISM: Rattus norvegicus

265 <400> SEQUENCE: 6

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270           20           25           30
272 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
273           35           40           45
275 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
276           50           55           60
278 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
279   65           70           75           80
281 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ser Gly Gln
282           85           90           95
284 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
285           100          105          110
287 Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
288           115          120          125
290 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
291           130          135          140
293 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
294  145          150          155          160
296 Gly Asn Pro Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
297           165          170          175
299 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
300           180          185          190
302 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
303           195          200          205
305 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
306           210          215          220
308 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
309  225          230          235          240
311 Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
312           245          250          255
314 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
315           260          265          270
317 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
318           275          280          285
320 Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
321           290          295          300
323 Thr Cys His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly
324  305          310          315          320
326 Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
327           325          330          335
329 Pro Ala Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala
330           340          345          350
332 Glu Gly Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/507,343

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Input Set : E:\405uspc.app.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; N Pos. 4,7,10,16,22

Seq#:26; Xaa Pos. 2,3,4,6,7,8,9,10,12,13,14,15,16,18,20,21,22,23,24,25,26

Seq#:26; Xaa Pos. 27,29,30,31,32

Seq#:27; Xaa Pos. 2,3,4,5,6,7,8,10,11,12,13,15,16,17,18,19,20,21,22,23,24

Seq#:27; Xaa Pos. 26,28,29,30,31,32,33,34,35

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:575 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:579 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1288 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
M:341 Repeated in SeqNo=26
L:1309 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1314 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27